SEQUENCE LISTING

<110> Thompson, John E.
      Wang, Tzann-Wei
      Lu, Dongen Lilly

<120> DNA ENCODING A PLANT DEOXYHYPUSINE SYNTHASE, TRANSGENIC
      PLANTS AND A METHOD FOR CONTROLLING PROGRAMMED CELL
      DEATH IN PLANTS

<130> 10799/9

<140>
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<150> 09/348,675
<151> 1999-07-06

<160> 35

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Lycopersicon sp.

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<222> (54..1196)

<220>
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gga gaa gct ctg aag tac agt atc atg gac tca gta aga tcg gta gtt   104
Gly Glu Ala Leu Lys Tyr Ser Ile Met Asp Ser Val Arg Ser Val Val
              5   10   15

ttc aaa gaa tcc gaa aat cta gaa ggt tct tgc act aaa atc gag ggc   152
Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu Gly
             20   25   30

tac gac ttc aat aaa ggc gtt aac tat gct gag ctg atc aag tcc atg   200
Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser Met
         35   40   45

gtt tcc act ggt ttc caa gca tct aat ctt ggt gac gcc att gca att   248
Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala Ile
 50   55   60   65

gtt aat caa atg cta gat tgg agg ctt tca cat gag ctg ccc acg gag   296
Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr Glu
                 70   75   80

gat tgc agt gaa gaa gaa aga gat gtt gca tac aga gag tcg gta acc   344
Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val Thr
             85   90   95

tgc aaa atc ttc ttg ggg ttc act tca aac ctt gtt tct tct ggt gtt   392
Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val

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aga gac act gtc cgc tac ctt gtt cag cac cgg atg gtt gat gtt gtg    440
Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val Val
    115                 120                 125

gtt act aca gct ggt ggt att gaa gag gat ctc ata aag tgc ctc gca    488
Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu Ala
130                 135                 140                 145

cca acc tac aag ggg gac ttc tct tta cct gga gct tct cta cga tcg    536
Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg Ser
                150                 155                 160

aaa gga ttg aac cgt att ggt aac tta ttg gtt cct aat gac aac tac    584
Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr
                165                 170                 175

tgc aaa ttt gag aat tgg atc atc cca gtt ttt gac caa atg tat gag    632
Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr Glu
            180                 185                 190

gag cag att aat gag aag gtt cta tgg aca cca tct aaa gtc att gct    680
Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile Ala
    195                 200                 205

cgt ctg ggt aaa gaa att aat gat gaa acc tca tac ttg tat tgg gct    728
Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp Ala
210                 215                 220                 225

tac aag aac cgg att cct gtc ttc tgt cct ggc ttg acg gat gga tca    776
Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser
                230                 235                 240

ctt ggt gac atg cta tac ttc cat tct ttc aaa aag ggt gat cca gat    824
Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro Asp
                245                 250                 255

aat cca gat ctt aat cct ggt cta gtc ata gac att gta gga gat att    872
Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp Ile
                260                 265                 270

agg gcc atg aat ggt gaa gct gtc cat gct ggt ttg agg aag aca gga    920
Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr Gly
    275                 280                 285

atg att ata ctg ggt gga ggg ctg cct aag cac cat gtt tgc aat gcc    968
Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Val Cys Asn Ala
290                 295                 300                 305

aat atg atg cgc aat ggt gca gat ttt gcc gtc ttc att aac acc gca    1016
Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr Ala
                310                 315                 320

caa gag ttt gat ggt agt gac tct ggt gcc cgt cct gat gaa gct gta    1064
Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val
                325                 330                 335

tca tgg gga aag ata cgt ggt ggt gcc aag act gtg aag gtg cat tgt    1112
Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His Cys
                340                 345                 350

gat gca acc att gca ttt ccc ata tta gta gct gag aca ttt gca gct    1160
Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala Ala
                355                 360                 365
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aag agt aag gaa ttc tcc cag ata agg tgc caa gtt tgaacattga        1206
Lys Ser Lys Glu Phe Ser Gln Ile Arg Cys Gln Val
370                 375             380

ggaagctgtc cttccgacca cacatatgaa ttgctagctt ttgaagccaa cttgctagtg   1266

tgcagcacca tttattctgc aaaactgact agagagcagg gtatattcct ctaccccgag   1326

ttagacgaca tcctgtatgg ttcaaattaa ttattttct cccccttcaca ccatgttatt   1386

tagttctctt cctcttcgaa agtgaagagc ttagatgttc ataggttttg aattatgttg   1446

gaggttggtg ataactgact agtcctctta ccatatagat aatgtatcct tgtactatga   1506

gattttgggt gtgtttgata ccaaggaaaa tgtttatttg gaaacaatt ggattttaa     1566

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<213> Lycopersicon sp.

<220>
<223> DHS

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Val Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu
                20                  25                  30

Gly Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser
            35                  40                  45

Met Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala
        50                  55                  60

Ile Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr
65                  70                  75                  80

Glu Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val
                85                  90                  95

Thr Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly
            100                 105                 110

Val Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val
        115                 120                 125

Val Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu
        130                 135                 140

Ala Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg
145                 150                 155                 160

Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn
                165                 170                 175

Tyr Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr
            180                 185                 190

Glu Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile
        195                 200                 205
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DC01 345180 v 1   3

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Ala Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp
    210                 215                 220

Ala Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly
225                 230                 235                 240

Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro
                245                 250                 255

Asp Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp
            260                 265                 270

Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr
        275                 280                 285

Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Val Cys Asn
    290                 295                 300

Ala Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr
305                 310                 315                 320

Ala Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala
                325                 330                 335

Val Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His
            340                 345                 350

Cys Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala
            355                 360                 365

Ala Lys Ser Lys Glu Phe Ser Gln Ile Arg Cys Gln Val
    370                 375                 380
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<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 3
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<210> 4
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 4
gactgcagtc gacatcgatt tttttttttt tttt   34

<210> 5
<211> 2272
<212> DNA
<213> Arabidopsis sp.

<220>
<221> CDS
<222> (68..265, 348..536, 624..842, 979..1065,
    1154..1258, 1575..1862)

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gagcaac atg gag gat gat cgt gtt ttc tct tcg gtt cac tca aca gtt   109
        Met Glu Asp Asp Arg Val Phe Ser Ser Val His Ser Thr Val
        1   5   10

ttc aaa gaa tcc gaa tca ttg gaa gga aag tgt gat aaa atc gaa gga   157
Phe Lys Glu Ser Glu Ser Leu Glu Gly Lys Cys Asp Lys Ile Glu Gly
15   20   25   30

tac gat ttc aat caa gga gta gat tac cca aag ctt atg cga tcc atg   205
Tyr Asp Phe Asn Gln Gly Val Asp Tyr Pro Lys Leu Met Arg Ser Met
                35   40   45

ctc acc acc gga ttt caa gcc tcg aat ctc ggc gaa gct att gat gtc   253
Leu Thr Thr Gly Phe Gln Ala Ser Asn Leu Gly Glu Ala Ile Asp Val
            50   55   60

gtc aat caa atg gttcgtttct cgaattcatc aaaaataaaa attccttctt   305
Val Asn Gln Met
            65

tttgttttcc tttgttttgg gtgaattagt aatgacaaag ag ttt gaa ttt gta   359
                                              Phe Glu Phe Val
                                                            70

ttg aag cta gat tgg aga ctg gct gat gaa act aca gta gct gaa gac   407
Leu Lys Leu Asp Trp Arg Leu Ala Asp Glu Thr Thr Val Ala Glu Asp
                75   80   85

tgt agt gaa gag gag aag aat cca tcg ttt aga gag tct gtc aag tgt   455
Cys Ser Glu Glu Glu Lys Asn Pro Ser Phe Arg Glu Ser Val Lys Cys
                90   95   100

aaa atc ttt cta ggt ttc act tca aat ctt gtt tca tct ggt gtt aga   503
Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val Arg
        105   110   115

gat act att cgt tat ctt gtt cag cat cat atg gtttgtgatt tttgctttat   556
Asp Thr Ile Arg Tyr Leu Val Gln His His Met
    120   125

caccctgctt ttttatagat gttaaaattt tcgagcttta gttttgattt caatggtttt   616

tctgcag gtt gat gtt ata gtc acg aca act ggt ggt gtt gag gaa gat   665
        Val Asp Val Ile Val Thr Thr Thr Gly Gly Val Glu Glu Asp
        130   135   140

ctc ata aaa tgc ctt gca cct aca ttt aaa ggt gat ttc tct cta cct   713
Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ser Leu Pro
    145   150   155

gga gct tat tta agg tca aag gga ttg aac cga att ggg aat ttg ctg   761
Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu
160   165   170   175

gtt cct aat gat aac tac tgc aag ttt gag gat tgg atc att ccc atc   809
Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile
                180   185   190

ttt gac gag atg ttg aag gaa cag aaa gaa gag gtattgcttt atctttcctt   862
Phe Asp Glu Met Leu Lys Glu Gln Lys Glu Glu
        195   200

tttatatgat ttgagatgat tctgtttgtg cgtcactagt ggagatagat tttgattcct   922

DC01 345180 v 1   5

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ctcttgcatc attgacttcg ttggtgaatc cttctttctc tggttttttcc ttgtag            978

aat gtg ttg tgg act cct tct aaa ctg tta gca cgg ctg gga aaa gaa          1026
Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys Glu
        205                 210                 215

atc aac aat gag agt tca tac ctt tat tgg gca tac aag gtatccaaaa           1075
Ile Asn Asn Glu Ser Ser Tyr Leu Tyr Trp Ala Tyr Lys
        220                 225                 230

ttttaacctt tttagttttt taatcatcct gtgaggaact cggggattta aattttccgc        1135

ttcttgtggt gtttgtag atg aat att cca gta ttc tgc cca ggg tta aca         1186
                    Met Asn Ile Pro Val Phe Cys Pro Gly Leu Thr
                            235                 240

gat ggc tct ctt ggg gat atg ctg tat ttt cac tct ttt cgt acc tct         1234
Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Arg Thr Ser
        245                 250                 255

ggc ctc atc atc gat gta gta caa ggtacttctt ttactcaata agtcagtgtg        1288
Gly Leu Ile Ile Asp Val Val Gln
        260                 265

ataaatattc ctgctacatc tagtgcagga atattgtaac tagtagtgca ttgtagcttt        1348

tccaattcag caacggactt tactgtaagt tgatatctaa aggttcaaac gggagctagg        1408

agaatagcat aggggcattc tgatttaggt ttggggcact gggttaagag ttagagaata        1468

ataatcttgt tagttgttta tcaaactctt tgatggttag tctcttggta atttgaattt        1528

tatcacagtg tttatggtct ttgaaccagt taatgtttta tgaaca gat atc aga          1583
                                                    Asp Ile Arg

gct atg aac ggc gaa gct gtc cat gca aat cct aaa aag aca ggg atg         1631
Ala Met Asn Gly Glu Ala Val His Ala Asn Pro Lys Lys Thr Gly Met
270                 275                 280                 285

ata atc ctt gga ggg ggc ttg cca aag cac cac ata tgt aat gcc aat         1679
Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn
                290                 295                 300

atg atg cgc aat ggt gca gat tac gct gta ttt ata aac acc ggg caa         1727
Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Gly Gln
                305                 310                 315

gaa ttt gat ggg agc gac tcg ggt gca cgc cct gat gaa gcc gtg tct         1775
Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val Ser
                320                 325                 330

tgg ggt aaa att agg ggt tct gct aaa acc gtt aag gtc tgc ttt tta         1823
Trp Gly Lys Ile Arg Gly Ser Ala Lys Thr Val Lys Val Cys Phe Leu
        335                 340                 345

att tct tca cat cct aat tta tat ctc act cag tgg ttt tgagtacata         1872
Ile Ser Ser His Pro Asn Leu Tyr Leu Thr Gln Trp Phe
350                 355                 360

tttaatattg gatcattctt gcaggtatac tgtgatgcta ccatagcctt cccattgttg        1932

gttgcagaaa catttgccac aaagagagac caaacctgtg agtctaagac ttaagaactg        1992

actggtcgtt ttggccatgg attcttaaag atcgttgctt tttgatttta cactggagtg        2052

accatataac actccacatt gatgtggctg tgacgcgaat tgtcttcttg cgaattgtac        2112
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tttagtttct ctcaacctaa aatgatttgc agattgtgtt ttcgtttaaa acacaagagt   2172

cttgtagtca ataatccttt gccttataaa attattcagt tccaacaaca cattgtgatt   2232

ctgtgacaag tctcccgttg cctatgttca cttctctgcg   2272

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<211> 362
<212> PRT
<213> Arabidopsis sp.

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                20   25   30

Phe Asn Gln Gly Val Asp Tyr Pro Lys Leu Met Arg Ser Met Leu Thr
            35   40   45

Thr Gly Phe Gln Ala Ser Asn Leu Gly Glu Ala Ile Asp Val Val Asn
        50   55   60

Gln Met Phe Glu Phe Val Leu Lys Leu Asp Trp Arg Leu Ala Asp Glu
65   70   75   80

Thr Thr Val Ala Glu Asp Cys Ser Glu Glu Glu Lys Asn Pro Ser Phe
                85   90   95

Arg Glu Ser Val Lys Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu
                100   105   110

Val Ser Ser Gly Val Arg Asp Thr Ile Arg Tyr Leu Val Gln His His
        115   120   125

Met Val Asp Val Ile Val Thr Thr Thr Gly Gly Val Glu Glu Asp Leu
    130   135   140

Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ser Leu Pro Gly
145   150   155   160

Ala Tyr Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val
                165   170   175

Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile Phe
            180   185   190

Asp Glu Met Leu Lys Glu Gln Lys Glu Glu Asn Val Leu Trp Thr Pro
        195   200   205

Ser Lys Leu Leu Ala Arg Leu Gly Lys Glu Ile Asn Asn Glu Ser Ser
    210   215   220

Tyr Leu Tyr Trp Ala Tyr Lys Met Asn Ile Pro Val Phe Cys Pro Gly
225   230   235   240

Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Arg
                245   250   255

Thr Ser Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg Ala Met Asn
            260   265   270

Gly Glu Ala Val His Ala Asn Pro Lys Lys Thr Gly Met Ile Ile Leu
        275   280   285

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Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met Met Arg
    290                 295                 300

Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Gly Gln Glu Phe Asp
305             310                 315                 320

Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys
            325                 330                 335

Ile Arg Gly Ser Ala Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser
        340                 345                 350

His Pro Asn Leu Tyr Leu Thr Gln Trp Phe
        355                 360


<210> 7
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 7
ggtggtgttg aggaagatc                                            19

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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ggtgcacgcc ctgatgaagc                                           20


<210> 9
<211> 1660
<212> DNA
<213> Dianthus sp.

<220>
<223> DHS

<220>
<221> CDS
<222> (256)..(1374)

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atactttgt ttttgacgtt tgataataat actatgaaaa tattatgttt tttcttttgt 120

gtgttggtgt ttttgaagtt gttttgata agcagaaccc agttgtttta cactttacc 180

attgaactac tgcaattcta aaactttgtt tacatttaa ttccatcaaa gattgagttc 240

agcataggaa aaagg atg gag gat gct aat cat gat agt gtg gca tct gcg 291
                  Met Glu Asp Ala Asn His Asp Ser Val Ala Ser Ala
                   1               5                  10

cac tct gca gca ttc aaa aag tcg gag aat tta gag ggg aaa agc gtt 339
His Ser Ala Ala Phe Lys Lys Ser Glu Asn Leu Glu Gly Lys Ser Val
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aag att gag ggt tat gat ttt aat caa ggt gta aac tat tcc aaa ctc   387
Lys Ile Glu Gly Tyr Asp Phe Asn Gln Gly Val Asn Tyr Ser Lys Leu
    30              35              40

ttg caa tct ttc gct tct aat ggg ttt caa gcc tcg aat ctt gga gat   435
Leu Gln Ser Phe Ala Ser Asn Gly Phe Gln Ala Ser Asn Leu Gly Asp
45              50              55              60

gcc att gaa gta gtt aat cat atg cta gat tgg agt ctg gca gat gag   483
Ala Ile Glu Val Val Asn His Met Leu Asp Trp Ser Leu Ala Asp Glu
                65              70              75

gca cct gtg gac gat tgt agc gag gaa gag agg gat cct aaa ttc aga   531
Ala Pro Val Asp Asp Cys Ser Glu Glu Glu Arg Asp Pro Lys Phe Arg
            80              85              90

gaa tct gtg aag tgc aaa gtg ttc ttg ggc ttt act tca aat ctt att   579
Glu Ser Val Lys Cys Lys Val Phe Leu Gly Phe Thr Ser Asn Leu Ile
        95              100             105

tcc tct ggt gtt cgt gac aca att cgg tat ctc gtg caa cat cat atg   627
Ser Ser Gly Val Arg Asp Thr Ile Arg Tyr Leu Val Gln His His Met
    110             115             120

gtt gac gtg ata gta acg aca acc gga ggt ata gaa gaa gat cta ata   675
Val Asp Val Ile Val Thr Thr Thr Gly Gly Ile Glu Glu Asp Leu Ile
125             130             135             140

aaa gga aga tcc atc aag tgc ctt gca ccc act ttc aaa ggc gat ttt   723
Lys Gly Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe
            145             150             155

gcc tta cca gga gct caa tta cgc tcc aaa ggg ttg aat cga att ggt   771
Ala Leu Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly
            160             165             170

aat ctg ttg gtt ccg aat gat aac tac tgt aaa ttt gag gat tgg atc   819
Asn Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile
            175             180             185

att cca att tta gat aag atg ttg gaa gag caa att tca gag aaa atc   867
Ile Pro Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile
    190             195             200

tta tgg aca cca tcg aag ttg att ggt cga tta gga aga gaa ata aac   915
Leu Trp Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn
205             210             215             220

gat gag agt tca tac ctt tac tgg gcc ttc aag aac aat att cca gta   963
Asp Glu Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val
            225             230             235

ttt tgc cca ggt tta aca gac ggc tca ctc gga gac atg cta tat ttt   1011
Phe Cys Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe
            240             245             250

cat tct ttt cgc aat ccg ggt tta atc gtc gat gtt gtg caa gat ata   1059
His Ser Phe Arg Asn Pro Gly Leu Ile Val Asp Val Val Gln Asp Ile
            255             260             265

aga gca gta aat ggc gag gct gtg cac gca gcg cct agg aaa aca ggc   1107
Arg Ala Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly
270             275             280
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atg att ata ctc ggt gga ggg ttg cct aag cac cac atc tgc aac gca   1155
Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala
285                 290                 295                 300

aac atg atg aga aat ggc gcc gat tat gct gtt ttc atc aac act gcc   1203
Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Ala
                    305                 310                 315

gaa gag ttt gac ggc agt gat tct ggt gct cgc ccc gat gag gct att   1251
Glu Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Ile
                320                 325                 330

tca tgg ggc aaa att agc gga tct gct aag act gtg aag gtg cat tgt   1299
Ser Trp Gly Lys Ile Ser Gly Ser Ala Lys Thr Val Lys Val His Cys
                335                 340                 345

gat gcc acg ata gct ttc cct cta cta gtc gct gag aca ttt gca gca   1347
Asp Ala Thr Ile Ala Phe Pro Leu Leu Val Ala Glu Thr Phe Ala Ala
        350                 355                 360

aaa aga gaa aaa gag agg aag agc tgt taaaactttt ttgattgttg         1394
Lys Arg Glu Lys Glu Arg Lys Ser Cys
365                 370

aaaaatctgt gttatacaag tctcgaaatg cattttagta attgacttga tcttatcatt 1454

tcaatgtgtt atctttgaaa atgttggtaa tgaaacatct cacctcttct atacaacatt 1514

gttgatccat tgtactccgt atcttgtaat tttggaaaaa aaaaccgtc tattgttacg  1574

agagagtaca tttttgaggt aaaaatatag gattttgtg cgatgcaaat gctggttatt  1634

cccttgaaaa aaaaaaaaaa aaaaaa                                       1660


<210> 10
<211> 373
<212> PRT
<213> Dianthus sp.

<220>
<223> DHS

<400> 10
Met Glu Asp Ala Asn His Asp Ser Val Ala Ser Ala His Ser Ala Ala
  1               5                  10                  15

Phe Lys Lys Ser Glu Asn Leu Glu Gly Lys Ser Val Lys Ile Glu Gly
             20                  25                  30

Tyr Asp Phe Asn Gln Gly Val Asn Tyr Ser Lys Leu Leu Gln Ser Phe
         35                  40                  45

Ala Ser Asn Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Glu Val
     50                  55                  60

Val Asn His Met Leu Asp Trp Ser Leu Ala Asp Glu Ala Pro Val Asp
 65                  70                  75                  80

Asp Cys Ser Glu Glu Glu Arg Asp Pro Lys Phe Arg Glu Ser Val Lys
                 85                  90                  95

Cys Lys Val Phe Leu Gly Phe Thr Ser Asn Leu Ile Ser Ser Gly Val
             100                 105                 110

Arg Asp Thr Ile Arg Tyr Leu Val Gln His His Met Val Asp Val Ile
```

DC01 345180 v 1   10

```
                115                      120                      125
    Val Thr Thr Thr Gly Gly Ile Glu Glu Asp Leu Ile Lys Gly Arg Ser
        130                 135                 140

    Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala Leu Pro Gly
    145                 150                 155                 160

    Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val
                    165                 170                 175

    Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile Leu
                180                 185                 190

    Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu Trp Thr Pro
                195                 200                 205

    Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp Glu Ser Ser
        210                 215                 220

    Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe Cys Pro Gly
    225                 230                 235                 240

    Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Arg
                    245                 250                 255

    Asn Pro Gly Leu Ile Val Asp Val Val Gln Asp Ile Arg Ala Val Asn
                260                 265                 270

    Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met Ile Ile Leu
                275                 280                 285

    Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met Met Arg
        290                 295                 300

    Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Ala Glu Glu Phe Asp
    305                 310                 315                 320

    Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Ile Ser Trp Gly Lys
                    325                 330                 335

    Ile Ser Gly Ser Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile
                340                 345                 350

    Ala Phe Pro Leu Leu Val Ala Glu Thr Phe Ala Ala Lys Arg Glu Lys
                355                 360                 365

    Glu Arg Lys Ser Cys
        370
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<210> 11
<211> 780
<212> DNA
<213> Lycopersicon sp.

<220>
<223> eif-5A

<220>
<221> CDS
<222> (43)..(522)

<400> 11
aaagaatcct agagagagaa agggaatcct agagagagaa gc atg tcg gac gaa   54
                                                Met Ser Asp Glu

```
gaa cac cat ttt gag tca aag gca gat gct ggt gcc tca aaa act ttc   102
Glu His His Phe Glu Ser Lys Ala Asp Ala Gly Ala Ser Lys Thr Phe
 5                  10                  15                  20

cca cag caa gct gga acc atc cgt aag aat ggt tac atc gtt atc aaa   150
Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile Val Ile Lys
                    25                  30                  35

ggc cgt ccc tgc aag gtt gtt gag gtc tcc act tca aaa act gga aaa   198
Gly Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys Thr Gly Lys
                40                  45                  50

cac gga cat gct aaa tgt cac ttt gtg gca att gac att ttc aat gga   246
His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile Phe Asn Gly
            55                  60                  65

aag aaa ctg gaa gat atc gtt ccg tcc tcc cac aat tgt gat gtg cca   294
Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys Asp Val Pro
        70                  75                  80

cat gtt aac cgt acc gac tat cag ctg att gat atc tct gaa gat ggt   342
His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser Glu Asp Gly
 85                  90                  95                 100

ttt gtc tca ctt ctt act gaa agt gga aac acc aag gat gac ctc agg   390
Phe Val Ser Leu Leu Thr Glu Ser Gly Asn Thr Lys Asp Asp Leu Arg
                   105                 110                 115

ctt ccc acc gat gaa aat ctg ctg aag cag gtt aaa gat ggg ttc cag   438
Leu Pro Thr Asp Glu Asn Leu Leu Lys Gln Val Lys Asp Gly Phe Gln
                   120                 125                 130

gaa gga aag gat ctt gtg gtg tct gtt atg tct gcg atg ggc gaa gag   486
Glu Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met Gly Glu Glu
               135                 140                 145

cag att aac gcc gtt aag gat gtt ggt acc aag aat tagttatgtc   532
Gln Ile Asn Ala Val Lys Asp Val Gly Thr Lys Asn
       150                 155                 160

atggcagcat aatcactgcc aaagctttaa gacattatca tatcctaatg tggtactttg   592

atatcactag attataaact gtgttatttg cactgttcaa aacaaaagaa agaaaactgc   652

tgttatggct agagaaagta ttggctttga cttttgaca gcacagttga actatgtgaa   712

aattctactt tttttttttt gggtaaaata ctgctcgttt aatgttttgc aaaaaaaaaa   772

aaaaaaaa                                                              780


<210> 12
<211> 160
<212> PRT
<213> Lycopersicon sp.

<220>
<223> eif-5A

<400> 12
Met Ser Asp Glu Glu His His Phe Glu Ser Lys Ala Asp Ala Gly Ala
 1               5                  10                  15


Ser Lys Thr Phe Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr
```

```
Ile Val Ile Lys Gly Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser
        35                    40                    45

Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp
    50                    55                    60

Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn
65                    70                    75                    80

Cys Asp Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile
            85                    90                    95

Ser Glu Asp Gly Phe Val Ser Leu Leu Thr Glu Ser Gly Asn Thr Lys
            100                   105                   110

Asp Asp Leu Arg Leu Pro Thr Asp Glu Asn Leu Leu Lys Gln Val Lys
        115                   120                   125

Asp Gly Phe Gln Glu Gly Lys Asp Leu Val Val Ser Val Met Ser Ala
        130                   135                   140

Met Gly Glu Glu Gln Ile Asn Ala Val Lys Asp Val Gly Thr Lys Asn
145                   150                   155                   160
```

<210> 13
<211> 812
<212> DNA
<213> Dianthus sp.

<220>
<223> eif-5A

<220>
<221> CDS
<222> (67)..(546)

<400> 13
ctcttttaca tcaatcgaaa aaaaattagg gttcttattt tagagtgaga ggcgaaaaat 60

```
cgaacg atg tcg gac gac gat cac cat ttc gag tca tcg gcc gac gcc      108
       Met Ser Asp Asp Asp His His Phe Glu Ser Ser Ala Asp Ala
        1               5                   10

gga gca tcc aag act tac cct caa caa gct ggt aca atc cgc aag agc      156
Gly Ala Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Ser
 15                  20                  25                  30

ggt cac atc gtc atc aaa aat cgc cct tgc aag gtg gtt gag gtt tct      204
Gly His Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser
                35                  40                  45

acc tcc aag act ggc aag cac ggt cat gcc aaa tgt cac ttt gtt gcc      252
Thr Ser Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala
            50                  55                  60

att gac att ttc aac ggc aag aag ctg gaa gat att gtc ccc tca tcc      300
Ile Asp Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser
        65                  70                  75

cac aat tgt gat gtt cca cat gtc aac cgt gtc gac tac cag ctg ctt      348
His Asn Cys Asp Val Pro His Val Asn Arg Val Asp Tyr Gln Leu Leu
    80                  85                  90
```

```
gat atc act gaa gat ggc ttt gtt agt ctg ctg act gac agt ggt gac    396
Asp Ile Thr Glu Asp Gly Phe Val Ser Leu Leu Thr Asp Ser Gly Asp
 95                 100                 105                 110

acc aag gat gat ctg aag ctt cct gct gat gag gcc ctt gtg aag cag    444
Thr Lys Asp Asp Leu Lys Leu Pro Ala Asp Glu Ala Leu Val Lys Gln
                115                 120                 125

atg aag gag gga ttt gag gcg ggg aaa gac ttg att ctg tca gtc atg    492
Met Lys Glu Gly Phe Glu Ala Gly Lys Asp Leu Ile Leu Ser Val Met
                130                 135                 140

tgt gca atg gga gaa gag cag atc tgc gcc gtc aag gac gtt agt ggt    540
Cys Ala Met Gly Glu Glu Gln Ile Cys Ala Val Lys Asp Val Ser Gly
        145                 150                 155

ggc aag tagaagcttt tgatgaatcc aatactacgc ggtgcagttg aagcaatagt    596
Gly Lys
        160

aatctcgaga acattctgaa ccttatatgt tgaattgatg gtgcttagtt tgttttggaa 656

atctctttgc aattaagttg taccaaatca atggatgtaa tgtcttgaat ttgttttatt 716

tttgttttga tgtttgctgt gattgcatta tgcattgtta tgagttatga cctgttataa 776

cacaaggttt tggtaaaaaa aaaaaaaaaa aaaaaa                             812


<210> 14
<211> 160
<212> PRT
<213> Dianthus sp.

<220>
<223> eif-5A

<400> 14
Met Ser Asp Asp Asp His His Phe Glu Ser Ser Ala Asp Ala Gly Ala
  1               5                  10                  15

Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Ser Gly His
                20                  25                  30

Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser
            35                  40                  45

Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp
     50                  55                  60

Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn
 65                  70                  75                  80

Cys Asp Val Pro His Val Asn Arg Val Asp Tyr Gln Leu Leu Asp Ile
                85                  90                  95

Thr Glu Asp Gly Phe Val Ser Leu Leu Thr Asp Ser Gly Asp Thr Lys
                100                 105                 110

Asp Asp Leu Lys Leu Pro Ala Asp Glu Ala Leu Val Lys Gln Met Lys
            115                 120                 125

Glu Gly Phe Glu Ala Gly Lys Asp Leu Ile Leu Ser Val Met Cys Ala
            130                 135                 140

Met Gly Glu Glu Gln Ile Cys Ala Val Lys Asp Val Ser Gly Gly Lys
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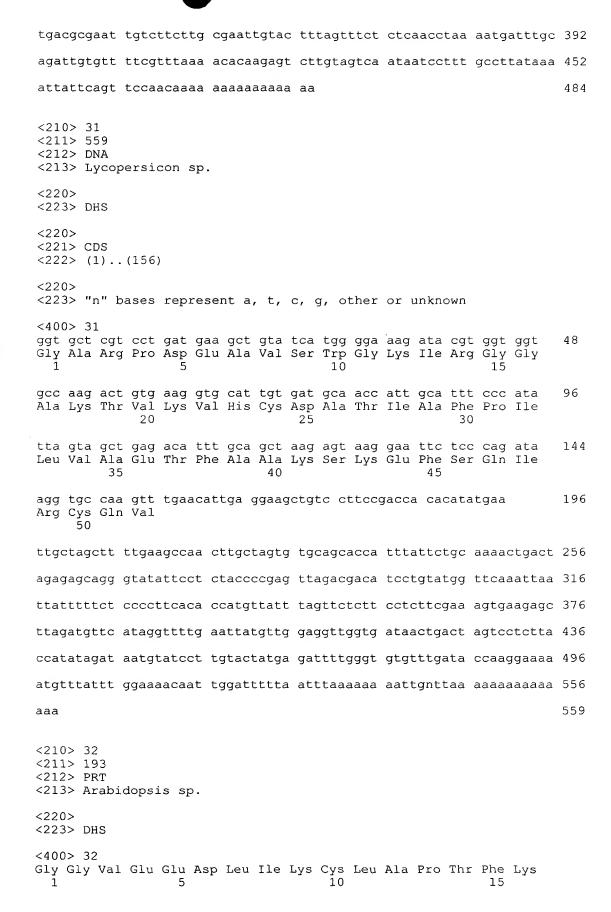
<210> 15
<211> 702
<212> DNA
<213> Arabidopsis sp.

<220>
<223> eif-5A

<220>
<221> CDS
<222> (56)..(529)

<400> 15
ctgttaccaa aaaatctgta ccgcaaaatc ctcgtcgaag ctcgctgctg caacc atg   58
                                                                Met
                                                                  1

tcc gac gag gag cat cac ttt gag tcc agt gac gcc gga gcg tcc aaa   106
Ser Asp Glu Glu His His Phe Glu Ser Ser Asp Ala Gly Ala Ser Lys
              5   10   15

acc tac cct caa caa gct gga acc atc cgt aag aat ggt tac atc gtc   154
Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile Val
          20   25   30

atc aaa aat cgt ccc tgc aag gtt gtt gag gtt tca acc tcg aag act   202
Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys Thr
      35   40   45

ggc aag cat ggt cat gct aaa tgt cat ttt gta gct att gat atc ttc   250
Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile Phe
  50   55   60   65

acc agc aag aaa ctc gaa gat att gtt cct tct tcc cac aat tgt gat   298
Thr Ser Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys Asp
                  70   75   80

gtt cct cat gtc aac cgt act gat tat cag ctg att gac att tct gaa   346
Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser Glu
              85   90   95

gat gga tat gtc agt ttg ttg act gat aac ggt agt acc aag gat gac   394
Asp Gly Tyr Val Ser Leu Leu Thr Asp Asn Gly Ser Thr Lys Asp Asp
          100   105   110

ctt aag ctc cct aat gat gac act ctg ctc caa cag atc aag agt ggg   442
Leu Lys Leu Pro Asn Asp Asp Thr Leu Leu Gln Gln Ile Lys Ser Gly
          115   120   125

ttt gat gat gga aaa gat cta gtg gtg agt gta atg tca gct atg gga   490
Phe Asp Asp Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met Gly
130   135   140   145

gag gaa cag atc aat gct ctt aag gac atc ggt ccc aag tgagactaac   539
Glu Glu Gln Ile Asn Ala Leu Lys Asp Ile Gly Pro Lys
                  150   155

aaagcctccc ctttgttatg agattcttct tcttctgtag gcttccatta ctcgtcggag   599

attatcttgt ttttgggtta ctcctatttt ggatatttaa actttgtta ataatgccat   659

cttcttcaac cttttccttc tagatggttt ttatacttct tct   702

<210> 16
<211> 158
<212> PRT
<213> Arabidopsis sp.

<220>
<223> eif-5A

<400> 16
Met Ser Asp Glu Glu His His Phe Glu Ser Ser Asp Ala Gly Ala Ser
 1   5   10   15

Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile
                20   25   30

Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys
            35   40   45

Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile
        50   55   60

Phe Thr Ser Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys
 65   70   75   80

Asp Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser
                85   90   95

Glu Asp Gly Tyr Val Ser Leu Leu Thr Asp Asn Gly Ser Thr Lys Asp
            100   105   110

Asp Leu Lys Leu Pro Asn Asp Asp Thr Leu Leu Gln Gln Ile Lys Ser
        115   120   125

Gly Phe Asp Asp Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met
    130   135   140

Gly Glu Glu Gln Ile Asn Ala Leu Lys Asp Ile Gly Pro Lys
145   150   155

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 17
aaarrycgmc cytgcaaggt   20

<210> 18
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
aatacgactc actatag   17

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<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<223> "n" bases represent a, t, c, g, other or unknown

<400> 19
tcyttnccyt cmkctaahcc                                              20


<210> 20
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
attaaccctc actaaag                                                 17


<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
ctgttaccaa aaaatctgta cc                                           22


<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 22
agaagaagta taaaaaccat c                                            21


<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 23
aaagaatcct agagagagaa agg                                          23


<210> 24
<211> 18
<212> DNA
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<210> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 24
ttttacatca atcgaaaa   18

<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 25
accaaaacct gtgttataac tcc   23

<210> 26
<211> 581
<212> DNA
<213> Arabidopsis sp.

<220>
<223> DHS

<220>
<221> CDS
<222> (1)..(579)

<400> 26
ggt ggt gtt gag gaa gat ctc ata aaa tgc ctt gca cct aca ttt aaa   48
Gly Gly Val Glu Glu Asp Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys
 1   5   10   15

ggt gat ttc tct cta cct gga gct tat tta agg tca aag gga ttg aac   96
Gly Asp Phe Ser Leu Pro Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn
            20   25   30

cga att ggg aat ttg ctg gtt cct aat gat aac tac tgc aag ttt gag   144
Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu
        35   40   45

gat tgg atc att ccc atc ttt gac gag atg ttg aag gaa cag aaa gaa   192
Asp Trp Ile Ile Pro Ile Phe Asp Glu Met Leu Lys Glu Gln Lys Glu
    50   55   60

gag aat gtg ttg tgg act cct tct aaa ctg tta gca cgg ctg gga aaa   240
Glu Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys
 65   70   75   80

gaa atc aac aat gag agt tca tac ctt tat tgg gca tac aag atg aat   288
Glu Ile Asn Asn Glu Ser Ser Tyr Leu Tyr Trp Ala Tyr Lys Met Asn
                85   90   95

att cca gta ttc tgc cca ggg tta aca gat ggc tct ctt agg gat atg   336
Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser Leu Arg Asp Met
            100   105   110

ctg tat ttt cac tct ttt cgt acc tct ggc ctc atc atc gat gta gta   384
Leu Tyr Phe His Ser Phe Arg Thr Ser Gly Leu Ile Ile Asp Val Val
        115   120   125

```
caa gat atc aga gct atg aac ggc gaa gct gtc cat gca aat cct aaa    432
Gln Asp Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Asn Pro Lys
    130             135             140

aag aca ggg atg ata atc ctt gga ggg ggc ttg cca aag cac cac ata    480
Lys Thr Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile
145             150             155             160

tgt aat gcc aat atg atg cgc aat ggt gca gat tac gct gta ttt ata    528
Cys Asn Ala Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile
            165             170             175

aac acc ggg caa gaa ttt gat ggg agc gac tcg ggt gca cgc cct gat    576
Asn Thr Gly Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp
            180             185             190

gaa gc                                                             581
Glu


<210> 27
<211> 522
<212> DNA
<213> Dianthus sp.

<220>
<223> DHS

<220>
<221> CDS
<222> (3)..(521)

<400> 27
ga aga tcc atc aag tgc ctt gca ccc act ttc aaa ggc gat ttt gcc     47
   Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala
   1               5               10              15

tta cca gga gct caa tta cgc tcc aaa ggg ttg aat cga att ggt aat    95
Leu Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn
            20              25              30

ctg ttg gtt ccg aat gat aac tac tgt aaa ttt gag gat tgg atc att   143
Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile
            35              40              45

cca att tta gat aag atg ttg gaa gag caa att tca gag aaa atc tta   191
Pro Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu
            50              55              60

tgg aca cca tcg aag ttg att ggt cga tta gga aga gaa ata aac gat   239
Trp Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp
    65              70              75

gag agt tca tac ctt tac tgg gcc ttc aag aac aat att cca gta ttt   287
Glu Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe
80              85              90              95

tgc cca ggt tta aca gac ggc tca ctc gga gac atg cta tat ttt cat   335
Cys Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His
            100             105             110

tct ttt cgc aat ccg ggt tta atc atc gat gtt gtg caa gat ata aga   383
Ser Phe Arg Asn Pro Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg
            115             120             125

gca gta aat ggc gag gct gtg cac gca gcg cct agg aaa aca ggc atg   431
```

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```
      Ala Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met
              130                 135                 140

      att ata ctc ggt gga ggg ttg cct aag cac cac atc tgc aac gca aac    479
      Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn
              145                 150                 155

      atg atg aga aat ggc gcc gat tat gct gtt ttc atc aac acc g          522
      Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr
      160                 165                 170


      <210> 28
      <211> 24
      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Description of Artificial Sequence: primer

      <400> 28
      ttgargaaga tycatmaart gcct                                          24


      <210> 29
      <211> 23
      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Description of Artificial Sequence: primer

      <400> 29
      ccatcaaayt cytgkgcrgt gtt                                           23


      <210> 30
      <211> 484
      <212> DNA
      <213> Arabidopsis sp.

      <220>
      <223> DHS

      <220>
      <221> CDS
      <222> (2)..(112)

      <400> 30
      t gca cgc cct gat gaa gct gtg tct tgg ggt aaa att agg ggt tct gct 49
        Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Ser Ala
        1                 5                   10                  15

      aaa acc gtt aag gtc tgc ttt tta att tct tca cat cct aat tta tat    97
      Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser His Pro Asn Leu Tyr
                      20                  25                  30

      ctc act cag tgg ttt tgagtacata tttaatattg gatcattctt gcaggtatac    152
      Leu Thr Gln Trp Phe
              35

      tgtgatgcta ccatagcctt cccattgttg gttgcagaaa catttgccac aaagagagac 212

      caaacctgtg agtctaagac ttaagaactg actggtcgtt ttggccatgg attcttaaag 272

      atcgttgctt tttgatttta cactggagtg accatataac actccacatt gatgtggctg 332
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tgacgcgaat tgtcttcttg cgaattgtac tttagtttct ctcaacctaa aatgatttgc 392

agattgtgtt ttcgtttaaa acacaagagt cttgtagtca ataatccttt gccttataaa 452

attattcagt tccaacaaaa aaaaaaaaaa aa 484

<210> 31
<211> 559
<212> DNA
<213> Lycopersicon sp.

<220>
<223> DHS

<220>
<221> CDS
<222> (1)..(156)

<220>
<223> "n" bases represent a, t, c, g, other or unknown

<400> 31
ggt gct cgt cct gat gaa gct gta tca tgg gga aag ata cgt ggt ggt   48
Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Gly
 1   5   10   15

gcc aag act gtg aag gtg cat tgt gat gca acc att gca ttt ccc ata   96
Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile Ala Phe Pro Ile
            20   25   30

tta gta gct gag aca ttt gca gct aag agt aag gaa ttc tcc cag ata   144
Leu Val Ala Glu Thr Phe Ala Ala Lys Ser Lys Glu Phe Ser Gln Ile
        35   40   45

agg tgc caa gtt tgaacattga ggaagctgtc cttccgacca cacatatgaa   196
Arg Cys Gln Val
    50

ttgctagctt ttgaagccaa cttgctagtg tgcagcacca tttattctgc aaaactgact 256

agagagcagg gtatattcct ctaccccgag ttagacgaca tcctgtatgg ttcaaattaa 316

ttattttct ccccttcaca ccatgttatt tagttctctt cctcttcgaa agtgaagagc 376

ttagatgttc ataggttttg aattatgttg gaggttggtg ataactgact agtcctctta 436

ccatatagat aatgtatcct tgtactatga gattttgggt gtgtttgata ccaaggaaaa 496

atgtttattt ggaaaacaat tggatttta atttaaaaaa aattgnttaa aaaaaaaaaa 556

aaa   559

<210> 32
<211> 193
<212> PRT
<213> Arabidopsis sp.

<220>
<223> DHS

<400> 32
Gly Gly Val Glu Glu Asp Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys
 1   5   10   15

```
Gly Asp Phe Ser Leu Pro Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn
            20                  25                  30

Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu
            35                  40                  45

Asp Trp Ile Ile Pro Ile Phe Asp Glu Met Leu Lys Glu Gln Lys Glu
        50                  55                  60

Glu Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys
65                  70                  75                  80

Glu Ile Asn Asn Glu Ser Ser Tyr Leu Tyr Trp Ala Tyr Lys Met Asn
                85                  90                  95

Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser Leu Arg Asp Met
                100                 105                 110

Leu Tyr Phe His Ser Phe Arg Thr Ser Gly Leu Ile Ile Asp Val Val
            115                 120                 125

Gln Asp Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Asn Pro Lys
        130                 135                 140

Lys Thr Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile
145                 150                 155                 160

Cys Asn Ala Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile
                165                 170                 175

Asn Thr Gly Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp
            180                 185                 190

Glu


<210> 33
<211> 173
<212> PRT
<213> Dianthus sp.

<220>
<223> DHS

<400> 33
Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala Leu
 1               5                  10                  15

Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu
            20                  25                  30

Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro
            35                  40                  45

Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu Trp
        50                  55                  60

Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp Glu
65                  70                  75                  80

Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe Cys
                85                  90                  95

Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser
                100                 105                 110
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Phe Arg Asn Pro Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg Ala
        115   120   125

Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met Ile
    130   135   140

Ile Leu Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met
145   150   155   160

Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr
            165   170

<210> 34
<211> 37
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<213> Arabidopsis sp.

<220>
<223> DHS

<400> 34
Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Ser Ala
 1   5   10   15

Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser His Pro Asn Leu Tyr
            20   25   30

Leu Thr Gln Trp Phe
        35

<210> 35
<211> 52
<212> PRT
<213> Lycopersicon sp.

<220>
<223> DHS

<400> 35
Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Gly
 1   5   10   15

Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile Ala Phe Pro Ile
            20   25   30

Leu Val Ala Glu Thr Phe Ala Ala Lys Ser Lys Glu Phe Ser Gln Ile
        35   40   45

Arg Cys Gln Val
        50